**METHODS**

*Study population*

The study data originated from the Cebu Longitudinal Health and Nutrition Survey (CLHNS), a longitudinal survey of 3,080 infants and their mothers who were recruited during their pregnancies between 1983-1984 in Metropolitan Cebu, Philippines. Out of the 1447 original female cohort infants, 823 were interviewed in a later 2009 survey (at ages 25-26). This additional survey tracked new pregnancies among these women between 2009-14. There were 383 who reported pregnancies (28% with 2-3 pregnancies) within the tracking period, yielding 507 pregnancy episodes. Women were visited in-home during pregnancy for anthropometric and questionnaire assessments, along with collection of a dried blood spot (DBS)—capillary whole blood collected on filter paper—for biomarker measurement. A second visit was arranged soon after delivery to obtain additional information from the mothers and to obtain phenotypic measures of their newborns. This research was conducted under conditions of written informed consent, and with approval of the Institutional Review Boards of Northwestern University (Evanston, Illinois), and the Office of Population Studies Foundation (Cebu, Philippines).

*Sample inclusion criteria*

Newborn anthropometric outcomes in these analyses included weight, length, head circumference, arm circumference, abdominal circumference, and sum of five skinfold thicknesses (triceps, subscapular, suprailiac, bicep and calf), which were measured in-home by trained interviewers using standardized procedures [reference later] as soon after birth as possible. The median and mean interval (in day) between birth and newborn anthropometry measurements were 3 and 4.5 days, respectively, with a range from 1 to 44 days. To minimize impacts of the infant’s environment and growth after birth, analyses of infants were limited to those measured within 2 weeks of birth and adjusted for age at measurement in models (this excluded 17 individuals measured more than 2 weeks after birth). Analyses were further limited to newborns born with gestational ages between 32 and 44 weeks, which excluded 5 very premature births and 2 implausibly late deliveries of around 46 weeks. Finally, only the oldest births for each of the women was included. After these exclusions, the final sample with all necessary biological and questionnaire data included 306 relatively healthy and unique singletons, Regression models were clustered on mother to account for non-independence among siblings (see below).

*Maternal covariates*

In each model, the gestational age at birth, fetal age at anthropometric measurement, fetal sex were all adjusted for. Because birth outcomes are potentially impacted by the mother’s adiposity, we also adjusted for the mother’s pre-pregnancy body mass index (BMI). Maternal socioeconomic status was measured using a pregnancy household assets scale reflecting whether the family had electricity, owned their home, owned an air conditioner, refrigerator, TV, vehicle and other appliances assessed, and a measure of household income that tallies all sources of income within the household (Adair et al 2011). Because women were enrolled in the birth outcome sub-study after they were pregnant, we used height and weight measurements collected during prior surveys to estimate pre-pregnancy BMI. We used 2009 BMI when available, and then used 2007 and 2005 data as necessary. Under the assumption that women will tend to maintain a stable position within the population BMI distribution even as the population mean increases with age, we converted all BMIs to age-specific within-sample Z-scores before pooling into a single pre-pregnancy BMI variable. Supporting the validity of this approach, the correlation between Z-scores for BMI measured in 2005 and 2009 was very high (r=0.84).

*Genome-wide DNA methylation analysis*

DNA was extracted from whole blood and assayed for DNA methylation by the UCLA Neurosciences Genomics Core using the Illumina Infinium HumanMethylation450 BeadChip (Illumina, Inc., San Diego, CA; 485, 577 CpG sites). DNA methylation data were pre-processed as per standard protocols.

*Calculation of epigenetic clocks*

The epigenetic age of the mothers emanating from their blood sample was calculated using previously established methods (cite later) and algorithms through the online DNA methylation calculator. The four primary epigenetic clocks were *intrinsic epigenetic age acceleration (IEAA), extrinstic epigenetic age acceleration (EEAA), phenotypic epigenetic age acceleration (PEAA), and GrimAgeAccel*. *IEAA* examines the intrinsic biological age of immune cells but does not depend on age-related changes in immune cells in the blood. *EEAA* captures immune cell biological age due to both intrinsic immune cell age and changes in immune cell populations in the blood. *PEAA* is determined using the Levine Method, which uses sites selected due to associations with phenotypic age indicators and chronological age. *GrimAgeAccel* is a marker enriched for DNA methylation sites that are surrogate markers for blood plasma proteins related to mortality. DNAm PAI-1, DNAm ADM, DNAm, B2M, DNAm cystatin C, DNAm GDF, DNAm leptin, DNAm TIMP1, and DNAm smoking pack years serve as these surrogate DNA methylation markers.

*Statistical analysis*

All statistical analyses were conducted using R. We ran a sequence of multivariate linear regression models designed to assess relationships between two fetal outcomes (gestational age and measured weight after birth) and the previously epigenetic age indices. Models predicting postnatal outcomes were adjusted for days after birth of anthropometry measurement, gestational age at birth, offspring gender, socioeconomic status, and pre-pregnancy BMI z-scores.